

G. SEQUENCE LISTING

5 (1) GENERAL INFORMATION

(i) APPLICANT: Darrell Anderson, Nabil Hanna, John Leonard,
Roland Newman and Mitchell Reff and William H.
Rastetter

10 (ii) TITLE OF INVENTION: THERAPEUTIC APPLICATION OF
CHIMERIC AND RADIOLABELED
ANTIBODIES TO HUMAN B
15 LYMPHOCYTE RESTRICTED
DIFFERENTIATION ANTIGEN FOR
TREATMENT OF B CELL LYMPHOMA

(iii) NUMBER OF SEQUENCES: 8

20 (iv) CORRESPONDING ADDRESS:

(A) ADDRESSEE: IDEC Pharmaceuticals Corporation
(B) STREET: 11011 Torreyana Road
(C) CITY: San Diego
25 (D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 92121

30 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
(B) COMPUTER: Macintosh
(C) OPERATING SYSTEM: MS.DOS
35 (D) SOFTWARE: Microsoft Word 5.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
40 (B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

45 (A) NAME: Burgoon, Richard P. Jr.
(B) REGISTRATION NUMBER: 34,787
(C) REFERENCE/DOCKET NUMBER:

(ix) TELECOMMUNICATION INFORMATION:

50 (A) TELEPHONE: (619) 550-8500
(B) TELEFAX: (619) 550-8750

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8540 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: yes

(iv) ANTI-SENSE: no

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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GACGTCGCGG CCGCTCTAGG CCTCCAAAAA AGCCTCCTCA CTACTTCTGG AATAGCTCAG 60
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ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCATACTTC TGCCTGCTGG GGAGCCTGGG 240
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GGGAGCCTG GGGACTTTCC ACACCCTAAC TGACACACAT TCCACAGAAT TAATCCCCCT 360
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ACGTCAATAA TGACGTATGT TCCCAGTAGA ACGCCAATAG GGACTTTCCA TTGACGTCAA 540
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TGCCTGCTGA ATAAGTTCTA TCCCAGAGAG GCCAAAGTAC AGTGGAAGGT GGATAACGCC 1200
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 25 GTAACAATC CGCCCCATTG ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA 2040
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 35 GGGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 2340
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 45 GAATACCCAG GCGTCCTCTC TGAGGTCCAG GAGGAAAAAG GCATCAAGTA TAAGTTTGAA 4500
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5 CTTCCGGAAG CGTGGCGCTT TCTCAATGCT CACGCTGTAG GTATCTCAGT TCGGTGTAGG 7020
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 30 GTTGCCGGGA AGCTAGAGTA AGTAGTTGCG CAGTTAATAG TTTGCGCAAC GTTGTGCCA 7860
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 50 GAATACTCAT ACTCTTCCTT TTTCAATATT ATTGAAGCAT TTATCAGGGT TATTGTCTCA 8460
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 55 TTCCCCGAAA AGTGCCACCT 8540

(3) INFORMATION FOR SEQ ID NO: 2:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9209 bases

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: circular

5 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: yes

10 (iv) ANTI-SENSE: no

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

15	GACGTCGCGG CCGCTCTAGG CCTCCAAAA AGCCTCCTCA CTACTTCTGG AATAGCTCAG	60
	AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAT TAGTCAGCCA TGCATGGGGC	120
	GGAGAATGGG CGGAAGTGGG CGGAGTTAGG GCGGGGATGG GCGGAGTTAG GGGCGGGACT	180
20	ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCATACTTC TGCCTGCTGG GGAGCCTGGG	240
	GACTTTCCAC ACCTGGTTGC TGAATAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT	300
25	GGGGAGCCTG GGGACTTTCC ACACCCTAAC TGACACACAT TCCACAGAAT TAATTCCCCT	360
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30	ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA	540
	TGGGTGGACT ATTTACGGTA AACTGCCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA	600
35	AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCG CCTGGCATTG TGCCCAGTAC	660
	ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC	720
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40	TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA AAATCAACGG	840
	GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG TAGGCGTGTA	900
45	CGGTGGGAGG TCTATATAAG CAGAGCTGGG TACGTGAACC GTCAGATCGC CTGGAGACGC	960
	CATCACAGAT CTCTCACTAT GGATTTTCAG GTGCAGATTA TCAGCTTCCT GCTAATCAGT	1020
	GCTTCAGTCA TAATGTCCAG AGGACAAATT GTTCTCTCCC AGTCTCCAGC AATCCTGTCT	1080
50	GCATCTCCAG GGGAGAAGGT CACAATGACT TGCAGGGCCA GCTCAAGTGT AAGTTACATC	1140
	CACTGGTTCC AGCAGAAGCC AGGATCCTCC CCCAAACCTT GGATTTATGC CACATCCAAC	1200
55	CTGGCTTCTG GAGTCCCTGT TCGCTTCAGT GGCAGTGGGT CTGGGACTTC TTA CTCTCTC	1260
	ACAATCAGCA GAGTGGAGGC TGAAGATGCT GCCACTTATT ACTGCCAGCA GTGGACTAGT	1320
	AACCCACCCA CGTTCGGAGG GGGGACCAAG CTGGAATCA AACGTACGGT GGCTGCACCA	1380
60	TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAAGTGC CTCTGTTGTG	1440

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 10 TGTGAATTC AGATCCGTTA ACGGTTACCA ACTACCTAGA CTGGATTCTG GACAACATGC 1740
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 15 TAATAAAATG AGGAAATTGC ATCGCATTGT CTGAGTAGGT GTCATTCTAT TCTGGGGGGT 1920
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 20 ACGTCAATGA CGGTAAATGG CCCGCCTGGC ATTATGCCA GTACATGACC TTATGGGACT 2100
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 25 GGCAGTACAT CAATGGGCGT GGATAGCGGT TTGACTCACG GGGATTCCA AGTCTCCACC 2220
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 35 GTACAACTGC AGCAGCCTGG GGCTGAGCTG GTGAAGCCTG GGGCCTCAGT GAAGATGTCC 2520
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 60 GAGGTCACAT GCGTGGTGGT GGACGTGAGC CACGAAGACC CTGAGGTCAA GTTCAACTGG 3300
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5 AGCACGTACC GTGTGGTCAG CGTCCTCACC GTCCTGCACC AGGACTGGCT GAATGGCAAG 3420
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 10 ~~CTGACGAAGA AGCAGCTCAG CCTGACCTGC CTGCTCAAAAG CCTTCTATCC GAGCGACATG~~ 3600
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 15 CAGCAGGGGA ACGTCTTCTC ATGCTCCGTG ATGCATGAGG CTCTGCACAA CCACTACACG 3780
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 20 CTTCTAGTTG CCAGCCATCT GTTGTGTTGCC CCTCCCCCGT GCCTTCCTTG ACCCTGGAAG 3960
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 25 GGTGTCATTC TATTCTGGGG GGTGGGGTGG GGCAGGACAG CAAGGGGGAG GATTGGGAAG 4080
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 30 AGGAAAATTA ATTTTAACAC CAATTCAGTA GTTGATTGAG CAAATGCGTT GCCAAAAGG 4260
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 ATTTGCGGCC AAACCTGACG GCAATCCTAG CGTGAAGGCT GGTAGGATTT TATCCCCGCT 4620
 45 GCCATCATGG TTCGACCATT GAACTGCATC GTCGCCGTGT CCCAAAATAT GGGGATTGGC 4680
 AAGAACGGAG ACCTACCCTG GCCTCCGCTC AGGAACGAGT TCAAGTACTT CCAAAGAATG 4740
 ACCACAACCT CTTCAGTGGA AGGTAAACAG AATCTGGTGA TTATGGGTAG GAAAACCTGG 4800
 50 TTCTCCATTC CTGAGAAGAA TCGACCTTTA AAGGACAGAA TTAATATAGT TCTCAGTAGA 4860
 GAACTCAAAG AACCACCACG AGGAGCTCAT TTTCTTGCCA AAAGTTTGGA TGATGCCTTA 4920
 55 AGACTTATTG AACAACCGGA ATTGGCAAGT AAAGTAGACA TGGTTTGGAT AGTCGGAGGC 4980
 AGTTCTGTTT ACCAGGAAGC CATGAATCAA CCAGGCCACC TTAGACTCTT TGTGACAAGG 5040
 ATCATGCAGG AATTTGAAAG TGACACGTTT TTCCAGAAA TTGATTTGGG GAAATATAAA 5100
 60 CTTCTCCCAG AATACCCAGG CGTCCTCTCT GAGGTCCAGG AGGAAAAAGG CATCAAGTAT 5160
 AAGTTTGAAG TCTACGAGAA GAAAGACTAA CAGGAAGATG CTTTCAAGTT CTCTGCTCCC 5220

CTCCTAAAGC TATGCATTTT TATAAGACCA TGGGACTTTT GCTGGCTTTA GATCAGCCTC 5280
 GACTGTGCCT TCTAGTTGCC AGCCATCTGT TGTTTGCCCC TCCCCCGTGC CTTCCCTTGAC 5340
 5 CCTGGAAGGT GCCACTCCCA CTGTCCTTTC CTAATAAAAT GAGGAAATTG CATCGCATTG 5400
 TCTGAGTAGG TGTCATTCTA TTCTGGGGGG TGGGGTGGGG CAGGACAGCA AGGGGGAGGA 5460
 10 TTGGGAAGAC AATAGCAGGC ATGCTGGGGA TGCGGTGGGC TCTATGGAAC CAGCTGGGGC 5520
 TCGAGCTACT AGCTTTGCTT CTCAATTTCT TATTTGCATA ATGAGAAAAA AAGGAAAATT 5580
 AATTTTAACA CCAATTCAGT AGTTGATTGA GCAAATGCGT TGCCAAAAAG GATGCTTTAG 5640
 15 AGACAGTGTT CTCTGCACAG ATAAGGACAA ACATTATTCA GAGGGAGTAC CCAGAGCTGA 5700
 GACTCCTAAG CCAGTGAGTG GCACAGCATT CTAGGGAGAA ATATGCTTGT CATCACCGAA 5760
 GCCTGATTCC GTAGAGCCAC ACCTTGGTAA GGGCCAATCT GCTCACACAG GATAGAGAGG 5820
 20 GCAGGAGCCA GGGCAGAGCA TATAAGGTGA GGTAGGATCA GTTGCTCCTC ACATTTGCTT 5880
 CTGACATAGT TGTGTTGGGA GCTTGGATCG ATCCTCTATG GTTGAACAAG ATGGATTGCA 5940
 25 CGCAGGTTCT CCGGCCGCTT GGGTGGAGAG GCTATTCGGC TATGACTGGG CACAACAGAC 6000
 AATCGGCTGC TCTGATGCCG CCGTGTTCCG GCTGTCAGCG CAGGGGCGCC CGGTTCTTTT 6060
 30 TGTCAGACC GACCTGTCCG GTGCCCTGAA TGAAGTGCAG GACGAGGCAG CGCGGCTATC 6120
 GTGGCTGGCC ACGACGGGCG TTCCTTGCGC AGCTGTGCTC GACGTTGTCA CTGAAGCGGG 6180
 AAGGGAAGTGG CTGCTATTGG GCGAAGTGCC GGGGCAGGAT CTCCTGTCTC CTCACCTTGC 6240
 35 TCCTGCCGAG AAAGTATCCA TCATGGCTGA TGCAATGCGG CGGCTGCATA CGCTTGATCC 6300
 GGCTACCTGC CCATTCGACC ACCAAGCGAA ACATCGCATC GAGCGAGCAC GTACTCGGAT 6360
 40 GGAAGCCGGT CTTGTGATC AGGATGATCT GGACGAAGAG CATCAGGGGC TCGCGCCAGC 6420
 CGAACTGTTC GCCAGGCTCA AGGCGCGCAT GCGGACGGC GAGGATCTCG TCGTGACCCA 6480
 TGGCGATGCC TGCTTGCCGA ATATCATGGT GGAAAATGGC CGCTTTTCTG GATTTCATCGA 6540
 45 CTGTGGCCGG CTGGGTGTGG CGGACCGCTA TCAGGACATA GCGTTGGCTA CCCGTGATAT 6600
 TGCTGAAGAG CTTGGCGGCG AATGGGCTGA CCGCTTCCTC GTGCTTTACG GTATCGCCGC 6660
 50 TCCCGATTCT CAGCGCATCG CCTTCTATCG CCTTCTTGAC GAGTCTTCT GAGCGGGACT 6720
 CTGGGGTTCT AAATGACCGA CCAAGCGAGC CCCAACCTGC CATCACGAGA TTTGATTCC 6780
 ACCGCCGCCT TCTATGAAAG GTTGGGCTTC GGAATCGTTT TCCGGGACGC CGGCTGGATG 6840
 55 ATCCTCCAGC GCGGGGATCT CATGCTGGAG TTCTTCGCCC ACCCAACTT GTTTATTGCA 6900
 GCTTATAATG GTTACAAATA AAGCAATAGC ATCACAAATT TCACAAATAA AGCATTTTTT 6960
 60 TCACTGCATT CTAGTTGTGG TTTGTCCAAA CTCATCAATC TATCTTATCA TGTCTGGATC 7020
 GCGGCCGCGA TCCCGTCGAG AGCTTGCGCT AATCATGGTC ATAGCTGTTT CCTGTGTGAA 7080
 ATTGTTATCC GCTCACAATT CCACACAACA TACGAGCCGG AAGCATAAAG TGTAAAGCCT 7140

	GGGGTGCCTA ATGAGTGAGC TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTTCC	7200
5	AGTCGGGAAA CCTGTCGTGC CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG	7260
	GTTTGCGTAT TGGGCGCTCT TCCGCTTCCT CGCTCACTGA CTCGCTGCGC TCGGTCGTTC	7320
	GGCTGCGGCG AGCGGTATCA GCTCACTCAA AGCGCGTAAT ACCTTTATCC ACAGAAATCA	7380
10	GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA AAAGGCCAGG AACCGTAAAA	7440
	AGGCCGCGTT GCTGGCGTTT TTCCATAGGC TCCGCCCCC TGACGAGCAT CACAAAAATC	7500
15	GACGCTCAAG TCAGAGGTGG CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTTCCCC	7560
	CTGGAAGCTC CCTCGTGCGC TCTCCTGTTC CGACCCTGCC GCTTACCGGA TACCTGTCCG	7620
	CCTTTCTCCC TTCGGGAAGC GTGGCGCTTT CTCAATGCTC ACGCTGTAGG TATCTCAGTT	7680
20	CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT GTGTGCACGA ACCCCCCGTT CAGCCCGACC	7740
	GCTGCGCCTT ATCCGGTAAC TATCGTCTTG AGTCCAACCC GGTAAGACAC GACTTATCGC	7800
25	CACTGGCAGC AGCCACTGGT AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG	7860
	AGTTCTTGAA GTGGTGGCCT AACTACGGCT AACTAGAAG GACAGTATTT GGTATCTGCG	7920
	CTCTGCTGAA GCCAGTTACC TTCGGAAGAA GAGTTGGTAG CTCTTGATCC GGCAAAACAA	7980
30	CCACCGCTGG TAGCGGTGGT TTTTTGTGT GCAAGCAGCA GATTACGCGC AGAAAAAAG	8040
	GATCTCAAGA AGATCCTTTG ATCTTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAAACT	8100
35	CACGTTAAGG GATTTTGGTC ATGAGATTAT CAAAAAGGAT CTTCACCTAG ATCCTTTTAA	8160
	ATTAAAAATG AAGTTTAAA TCAATCTAAA GTATATATGA GTAAACTTGG TCTGACAGTT	8220
	ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG TCTATTTCTG TCATCCATAG	8280
40	TTGCCTGACT CCCCCTCGTG TAGATAACTA CGATACGGGA GGGCTTACCA TCTGGCCCCA	8340
	GTGCTGCAAT GATACCGCGA GACCCACGCT CACCGGCTCC AGATTTATCA GCAATAAACC	8400
45	AGCCAGCCGG AAGGGCCGAG CGCAGAAGTG GTCCTGCAAC TTTATCCGCC TCCATCCAGT	8460
	CTATTAATTG TTGCCGGGAA GCTAGAGTAA GTAGTTCGCC AGTTAATAGT TTGCGCAACG	8520
	TTGTTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTTGGTATG GCTTCATTCA	8580
50	GCTCCGGTTC CCAACGATCA AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG	8640
	TTAGCTCCTT CGGTCCTCCG ATCGTTGTCA GAAGTAAGTT GGCCGCAGTG TTATCACTCA	8700
55	TGTTTATGGC AGCACTGCAT AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG	8760
	TGACTGGTGA GTACTCAACC AAGTCATTCT GAGAATAGTG TATGCGGCGA CCGAGTTGCT	8820
	CTTGCCCGGC GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA	8880
60	TCATTGGAAA ACGTTCTTCG GGGCGAAAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA	8940
	GTTTCATGTA ACCCACTCGT GCACCAAACT GATCTTCAGC ATCTTTTACT TTCACCAGCG	9000

TTTCTGGGTG AGCAAAAACA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC 9060
 GGAAATGTTG AATACTCATA CTCTTCCTTT TTCAATATTA TTGAAGCATT TATCAGGGTT 9120
 5 ATTGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA AAATAAACAA ATAGGGGTTT 9180
 CGCGCACATT TCCCCGAAAA GTGCCACCT 9209

10 (4) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 54 bases
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: yes

(iv) ANTI-SENSE: no

25 (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

5' ATC ACA GAT CTC TCA CCA TGG ATT TTC AGG TBC AGA TTA TCA GCT 52
 TC 3' 2

30 (5) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 30 bases
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: yes

(iv) ANTI-SENSE: yes

45 (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

50 5' TGC AGC ATC CGT ACG TTT GAT TTC CAG CTT 3' 30

(6) INFORMATION FOR SEQ ID NO: 5:

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 384 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: yes

10

(iv) ANTI-SENSE: no

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

15 ATG GAT TTT CAG GTG CAG ATT ATC AGC TTC CTG CTA ATC AGT GCT TCA GTC 51
ATA ATG TCC AGA GGG CAA ATT GTT CTC TCC CAG TCT CCA GCA ATC CTG TCT 102
GCA TCT CCA GGG GAG AAG GTC ACA ATG ACT TGC AGG GCC AGC TCA AGT GTA 153
20 AGT TAC ATC CAC TGG TTC CAG CAG AAG CCA GGA TCC TCC CCC AAA CCC TGG 204
ATT TAT GCC ACA TCC AAC CTG GCT TCT GGA GTC CCT GTT CGC TTC AGT GGC 255
25 AGT GGG TCT GGG ACT TCT TAC TCT CTC ACA ATC AGC AGA GTG GAG GCT GAA 306
GAT GCT GCC ACT TAT TAC TGC CAG CAG TGG ACT AGT AAC CCA CCC ACG TTC 357
GGA GGG GGG ACC AAG CTG GAA ATC AAA 384
30

(7) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 27 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: yes

45

(iv) ANTI-SENSE: no

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

50

5' GCG GCT CCC ACG CGT GTC CTG TCC CAG 3'

27

(8) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 29 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: yes

(iv) ANTI-SENSE: yes

15 (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

5' GGS TGT TGT GCT AGC TGM RGA GAC RGT GA 3' 29

20 (9) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 420 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: yes

(iv) ANTI-SENSE: no

35 (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

40 ATG GGT TGG AGC CTC ATC TTG CTC TTC CTT GTC GCT GTT GCT ACG CGT GTC 51
CTG TCC CAG GTA CAA CTG CAG CAG CCT GGG GCT GAG CTG GTG AAG CCT GGG 102
GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTT ACC AGT TAC 153
45 AAT ATG CAC TGG GTA AAA CAG ACA CCT GGT CGG GGC CTG GAA TGG ATT GGA 204
GCT ATT TAT CCC GGA AAT GGT GAT ACT TCC TAC AAT CAG AAG TTC AAA GGC 255
AAG GCC ACA TTG ACT GCA GAC AAA TCC TCC AGC ACA GCC TAC ATG CAG CTC 306
50 AGC AGC CTG ACA TCT GAG GAC TCT GCG GTC TAT TAC TGT GCA AGA TCG ACT 357
TAC TAC GGC GGT GAC TGG TAC TTC AAT GTC TGG GGC GCA GGG ACC ACG GTC 408
ACC GTC TCT GCA 420